1 Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro Leu Glu Glu Ala
1 CAG AGG TTG CCC CGG ATG CAG GAG GAT TCC CCC TTG GAG GAG GCT

16 Leu Leu Gly Lys Met Thr His Trp Ala Arg Arg Ile Cys Pro Val
46 CTT CTG GGG AAG ATG ACC CAC TGG GCG AGG AGG ATC TGC CCA GTG

31 Lys Arg Ile His Pro Glu Arg Arg Ile His Pro Glu Arg Arg Ile
91 AAG AGG ATT CAC CCA GAG AGG AGG ATC CAC CCG GAG AGG AGG ATC

46 Tyr Leu Glu Arg Arg Ile Tyr Leu Glu Arg Arg Ile Tyr Leu Lys
136 TAC CTG GAG AGG AGG ATC TAC CTG GAG AGG AGG ATC TAC CTG AAG

61 Leu Met Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp
181 TTA ATG CCT AAA TCA GAA GAA GAG GGC TCC CTG AAG TTA GAG GAT

76 Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn
226 CTA CCT ACT GTT GAG GCT CCT GGA GAT CCT CAA GAA CCC CAG AAT

91 Asn Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp Arg
271 AAT GCC CAC AGG GAC AAA GAA GGG GAT GAC CAG AGT CAT TGG CGC

106 Tyr Gly Gly Asp Pro Pro Gly Pro Gly Cys Pro Gln Pro Ala Arg
316 TAT GGA GGC GAC CCG CCT GGC CCC GGG TGT CCC CAG CCT GCG CGG

121 Ala Ala Ser Ser Pro Arg Trp Ile Ser Ala Pro Ser Ser Pro Pro
361 GCC GCT TCC AGT CCC CGG TGG ATA TCC GCC CCC AGC TCG CCG CCT

136 Ser Ala Arg Pro Cys Ala Pro Trp Asn Ser Trp Ala Ser Ser Ser
406 TCT GCC CGG CCC TGC GCC CCC TGG AAC TCC TGG GCT TCC AGC TCC

151 Arg Arg Ser Gln Asn Cys Ala Cys Arg Gln Trp Pro Gln Cys Ala
451 CGC CGC TCC CAG AAC TGC GCC TGC AGA CAA TGG CCA CAG TGT GCA

166 Thr Asp Pro Ala Ser Trp Ala Arg Asp Gly Ser Gly Ser Arg Ala
496 ACT GAC CCT GCC TCC TGG GCT AGA GAT GGC TCT GGG TCC CGG GCG

181 Gly Val Pro Ala Leu Gln Leu His Leu His Trp Gly Ala Ala Gly
541 GGA GTA CCG GCT CTG CAG CTG CAT CTG CAC TGG GGG GCT GCA GGT

196 Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg Phe Pro Ala
586 CGT CCG GGC TCG GAG CAC ACT GTG GAA GGC CAC CGT TTC CCT GCC

211 Glu Ile His Val Val His Leu Ser Thr Ala Phe Ala Arg Val Asp
631 GAG ATC CAC GTG GTT CAC CTC AGC ACC GCC TTT GCC AGA GTT GAC

226 Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Pro Phe
676 GAG GCC TTG GGG CGC CCG GGA GGC CTG GCC GTG TTG GCG CCT TTC

FIG. 1A

241 Trp Arg Arg Ala Arg Lys Lys Thr Val Ser Tyr Glu Gln Leu Leu
721 TGG AGG AGG GCC CGG AAG AAA ACA GTG TCC TAT GAG CAG TTG CTG

256 Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser Glu Thr Gln Val
766 TCT CGC TTG GAA GAA ATC GCT GAG GAA GGC TCA GAG ACT CAG GTC

271 Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp Phe Ser Arg
811 CCA GGA CTG GAC ATA TCT GCA CTC CTG CCC TCT GAC TTC AGC CGC

286 Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ala Gln
856 TAC TTC CAA TAT GAG GGG TCT CTG ACT ACA CCG CCC TGT GCC CAG

301 Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser Ala
901 GGT GTC ATC TGG ACT GTG TTT AAC CAG ACA GTG ATG CTG AGT GCT

316 Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp
946 AAG CAG CTC CAC ACC CTC TCT GAC ACC CTG TGG GGA CCT GGT GAC

331 Ser Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly
991 TCT CGG CTA CAG CTG AAC TTC CGA GCG ACG CAG CCT TTG AAT GGG

346 Arg Val Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser Pro
1036 CGA GTG ATT GAG GCC TCC TTC CCT GCT GGA GTG GAC AGC AGT CCT

361 Arg Ala Ala Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly
1081 CGG GCT GCT GAG CCA GTC CAG CTG AAT TCC TGC CTG GCT GCT GGT

376 Asp Ile Leu Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser
1126 GAC ATC CTA GCC CTG GTT TTT GGC CTC CTT TTT GCT GTC ACC AGC

391 Val Ala Phe Leu Val Gln Met Arg Arg Gln His Arg Arg Gly Thr
1171 GTC GCG TTC CTT GTG CAG ATG AGA AGG CAG CAC AGA AGG GGA ACC

406 Lys Gly Gly Val Ser Val Pro Pro Ser Arg Gly Ser Arg Asp Trp
1216 AAA GGG GGT GTG AGC GTA CCG CCC AGC AGA GGT AGC CGA GAC TGG

421 Ser Leu Glu Ala Gly Ser Trp Arg Met ***
1261 AGC CTA GAG GCT GGA TCT TGG AGA ATG TGA GAA GCC AGC CAG AGG

1306 CAT CTG AGG GGG AGC CGG TAA CTG TCC TGT CCT GCT CAT TAT GCC

1351 ACT TCC TTT TAA CTG CCA AGA AAT TTT TTA AAA TAA ATA TTT ATA

1396 AT

FIG. 1 B

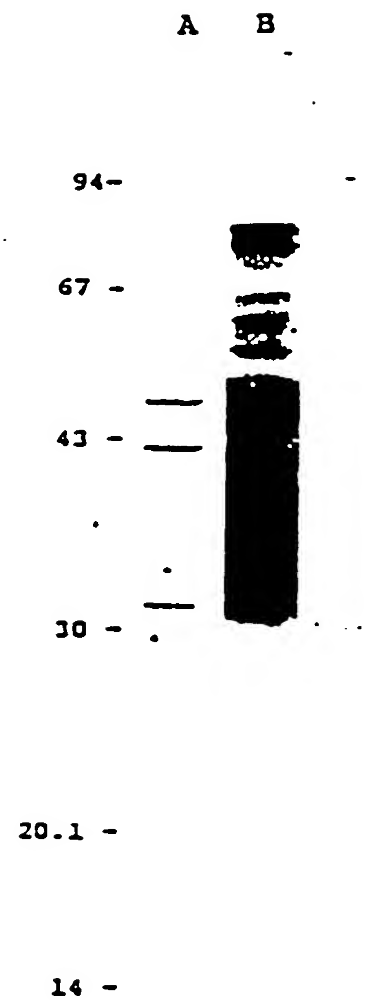


FIG. 2

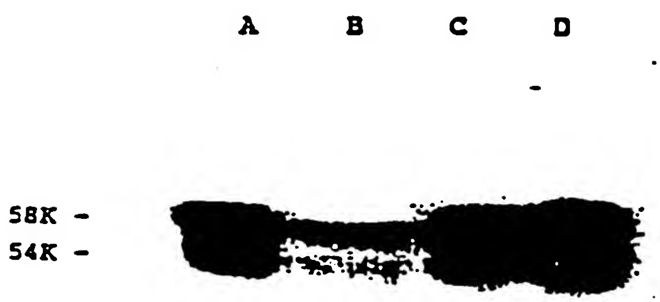


FIG. 3

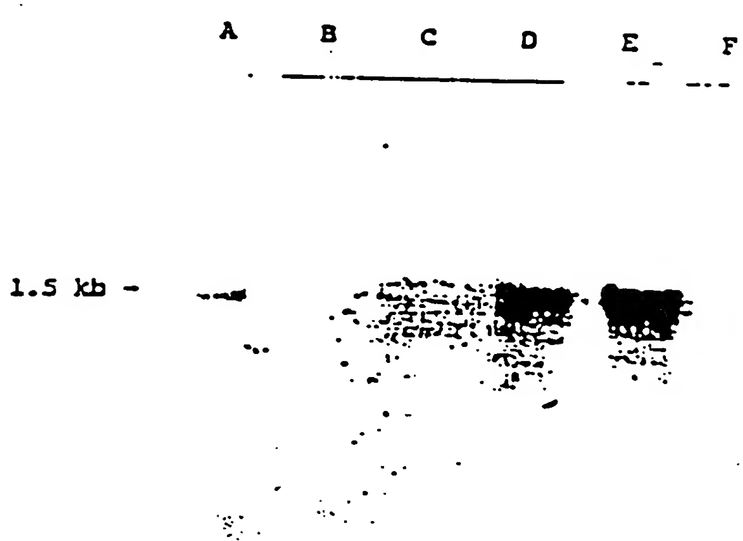


FIG. 4

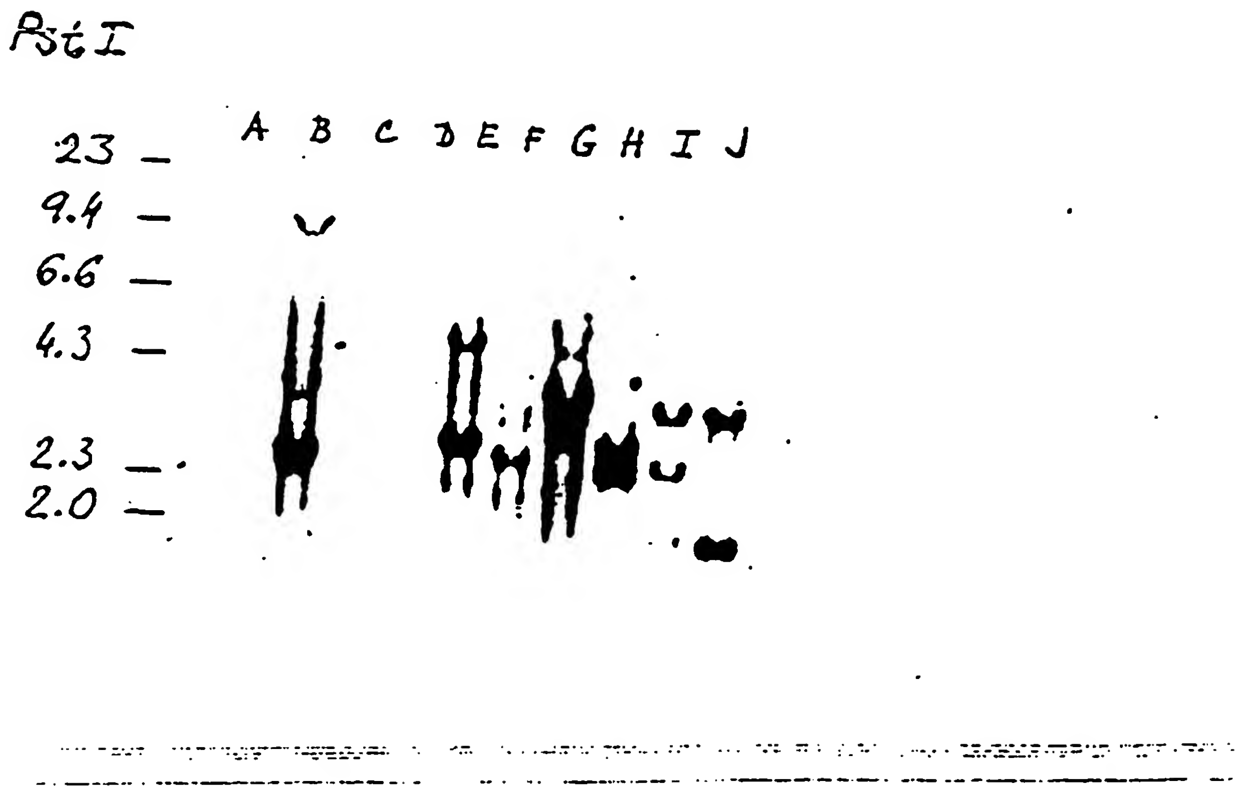


FIG. 5

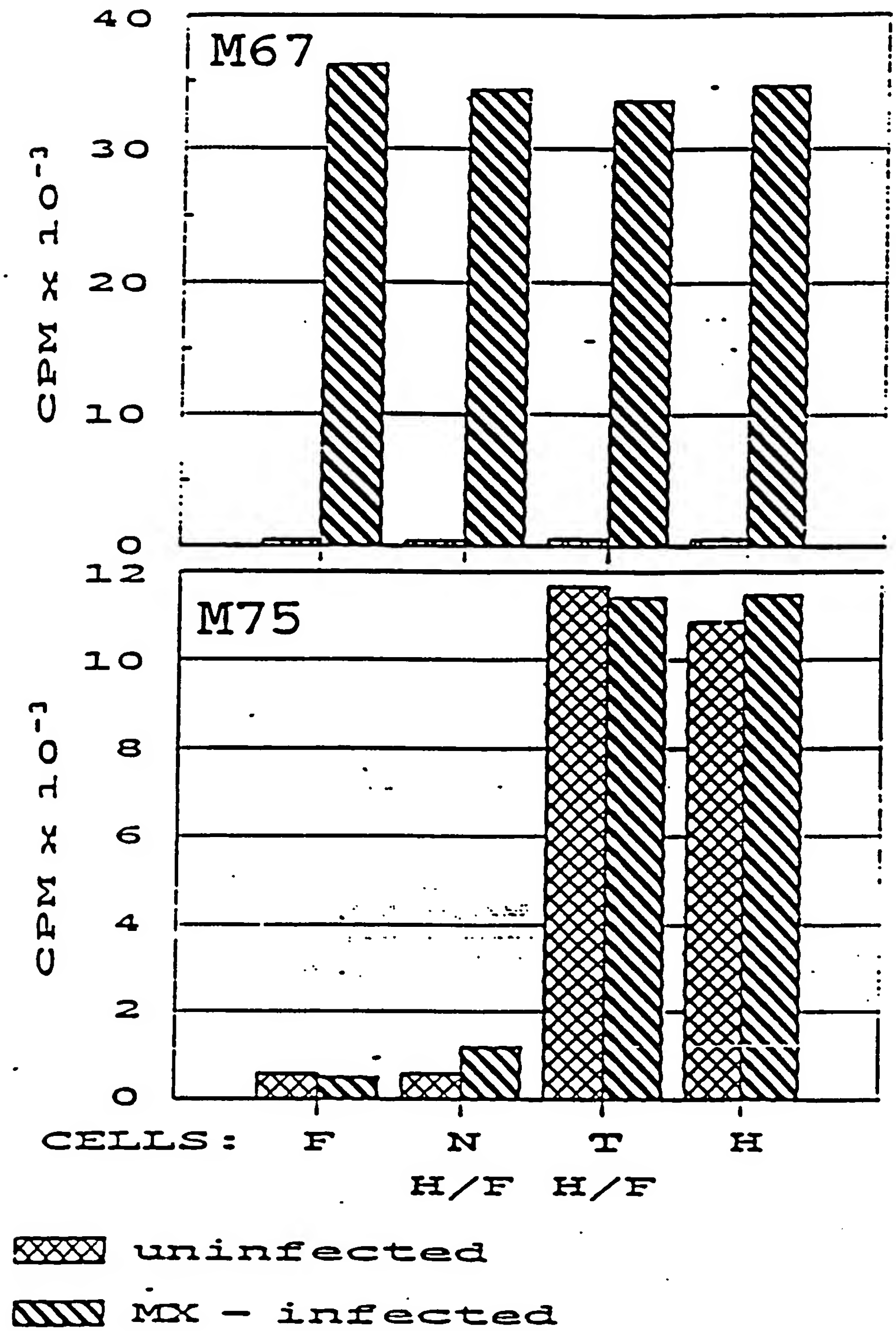

M67
M75
40
30
20
10
0
12
10
8
6
4
2
0
CPM x 10⁻¹
CELLS:
F
N
T
H
H/F
H/F
uninfected
MX - infected

FIG. 6

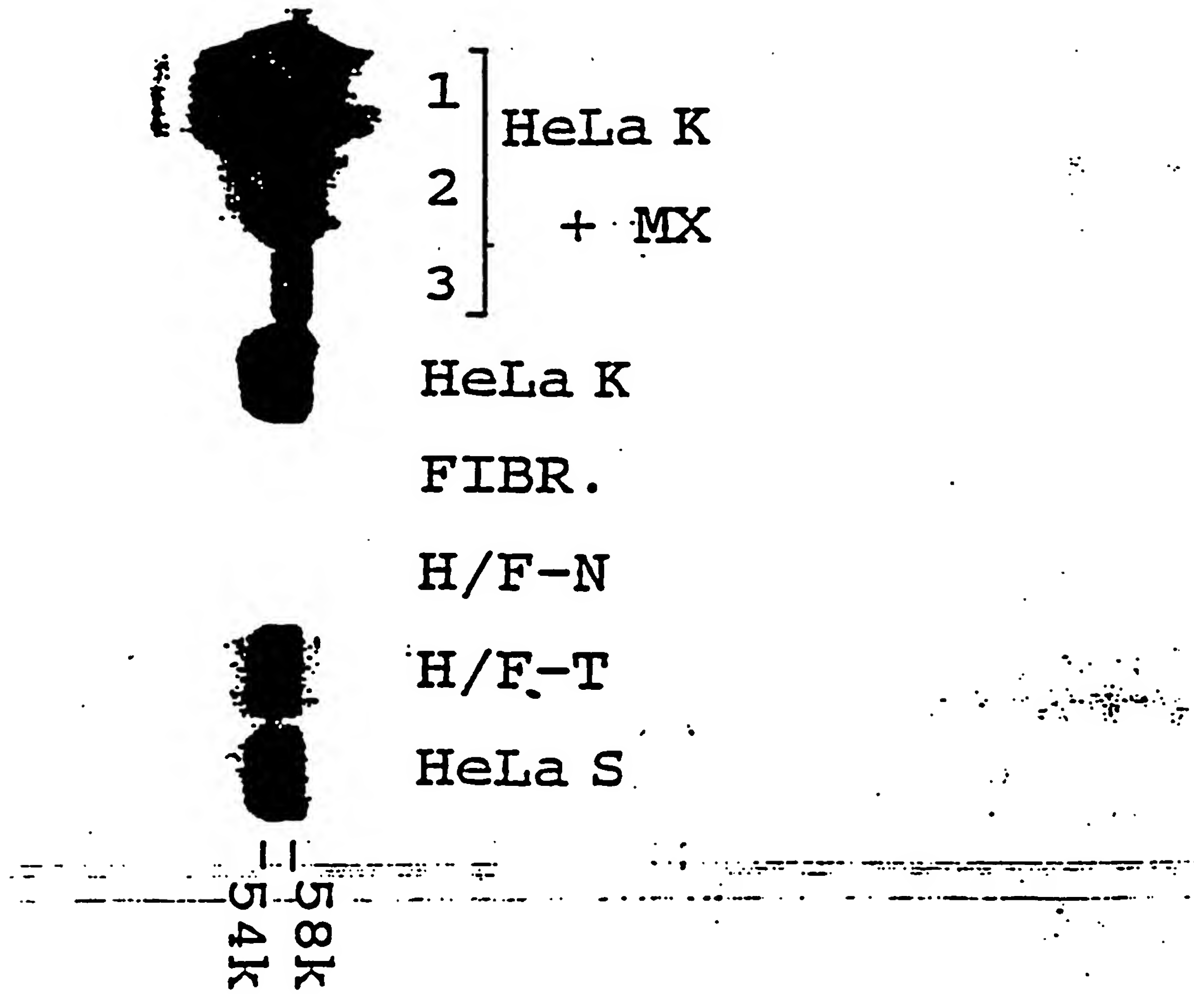


FIG. 7

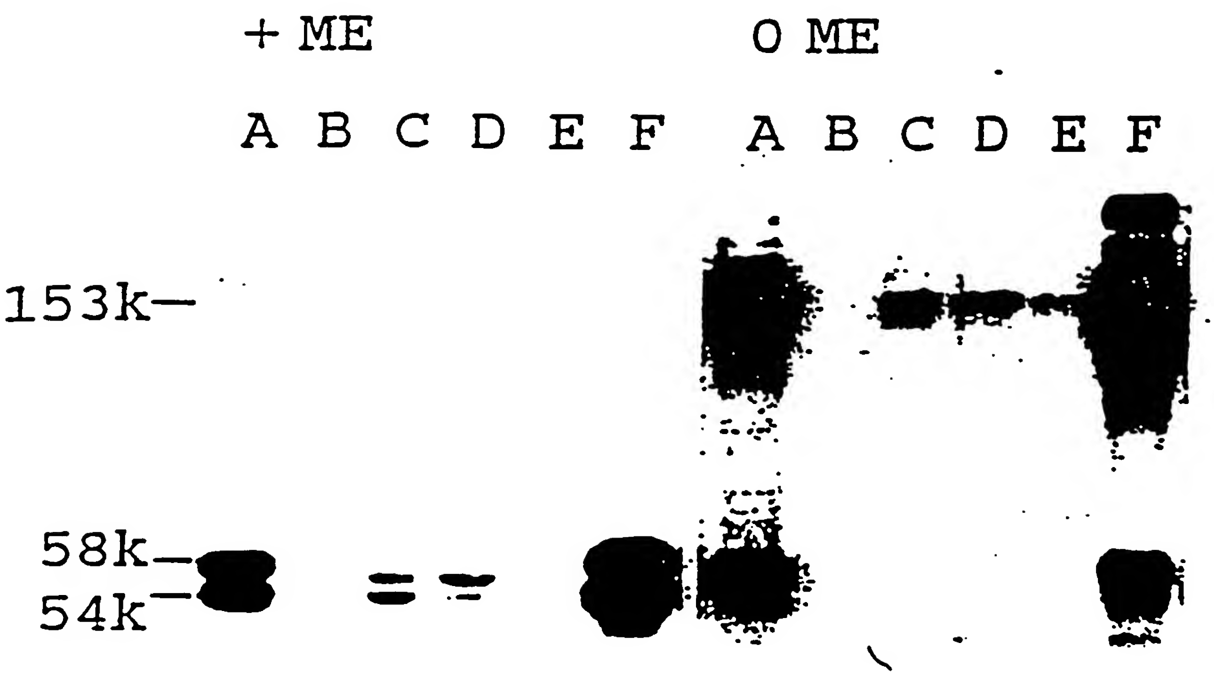


FIG. 8

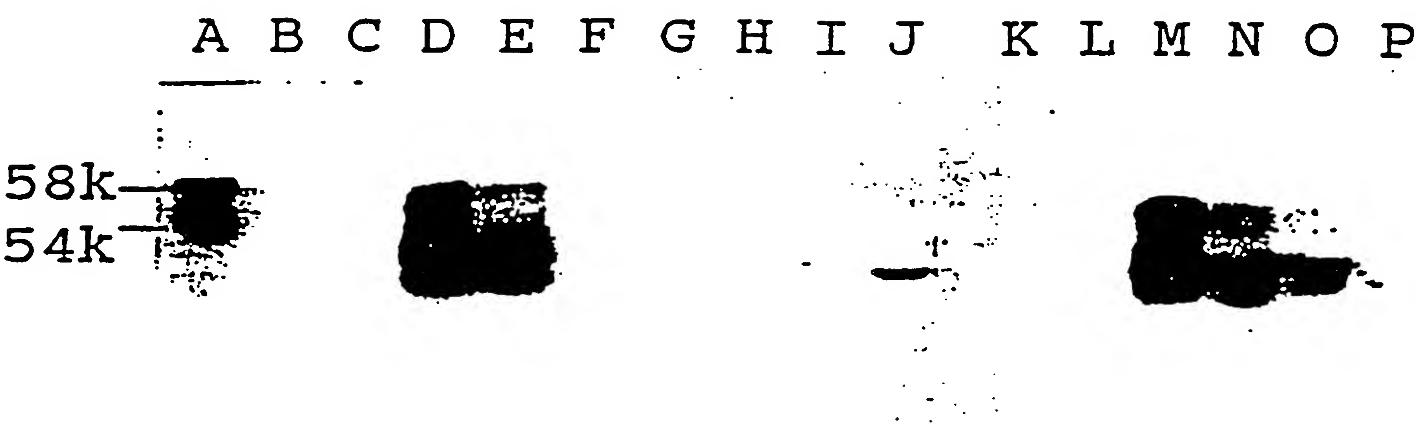


FIG. 9

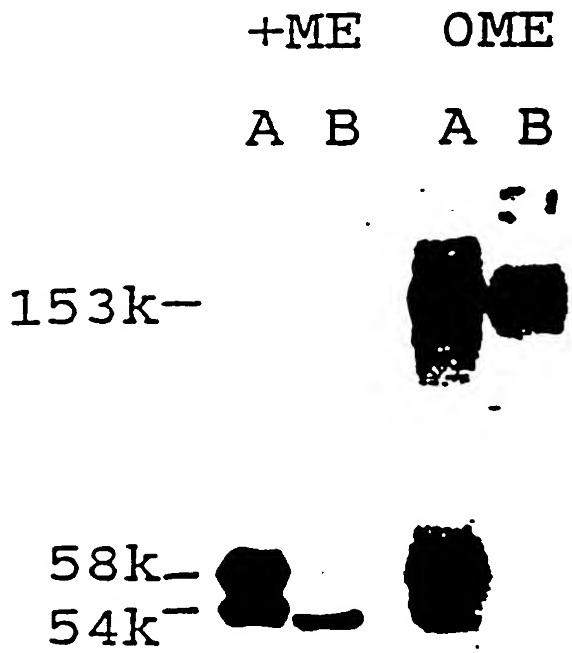


FIG. 10

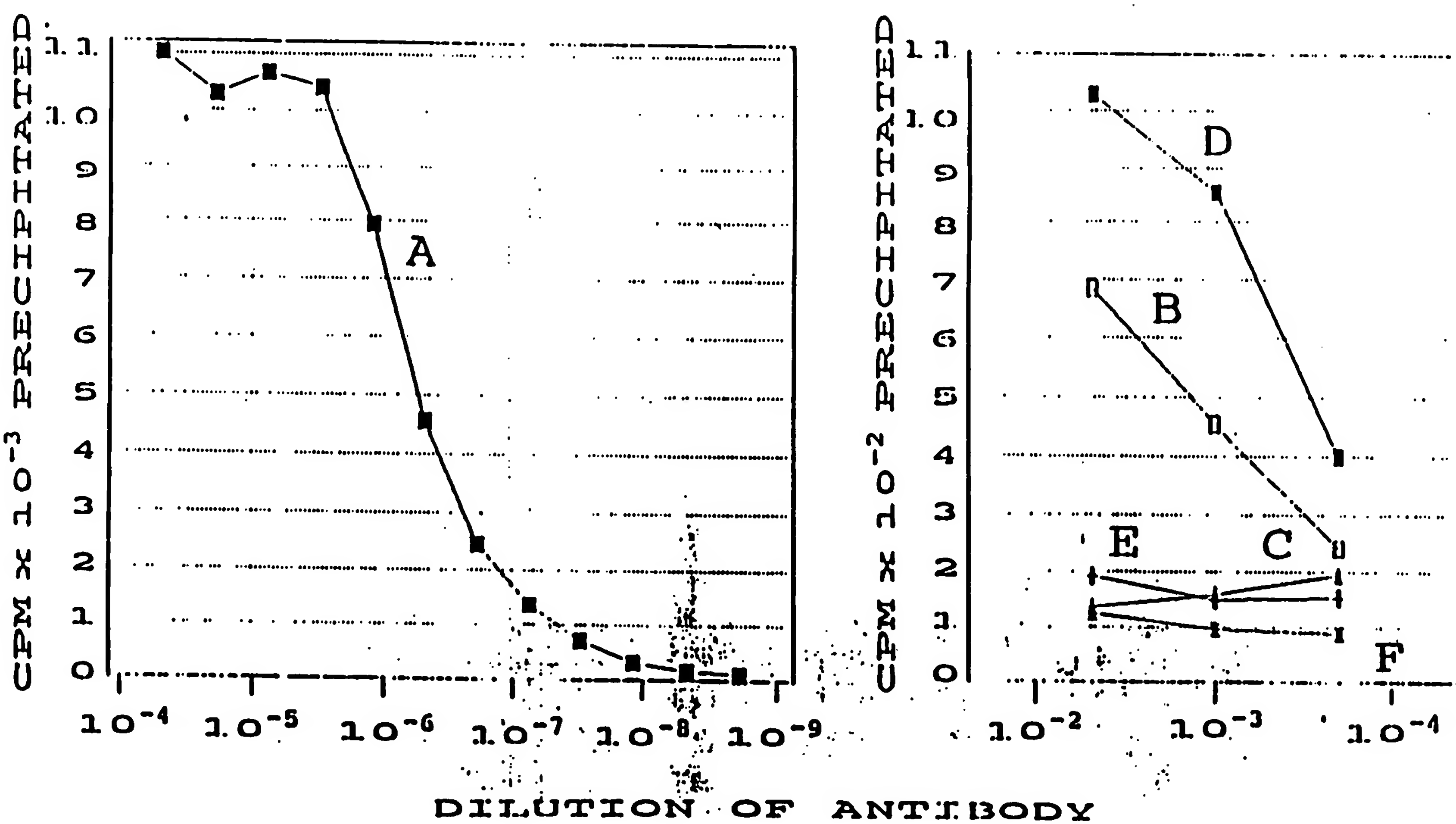
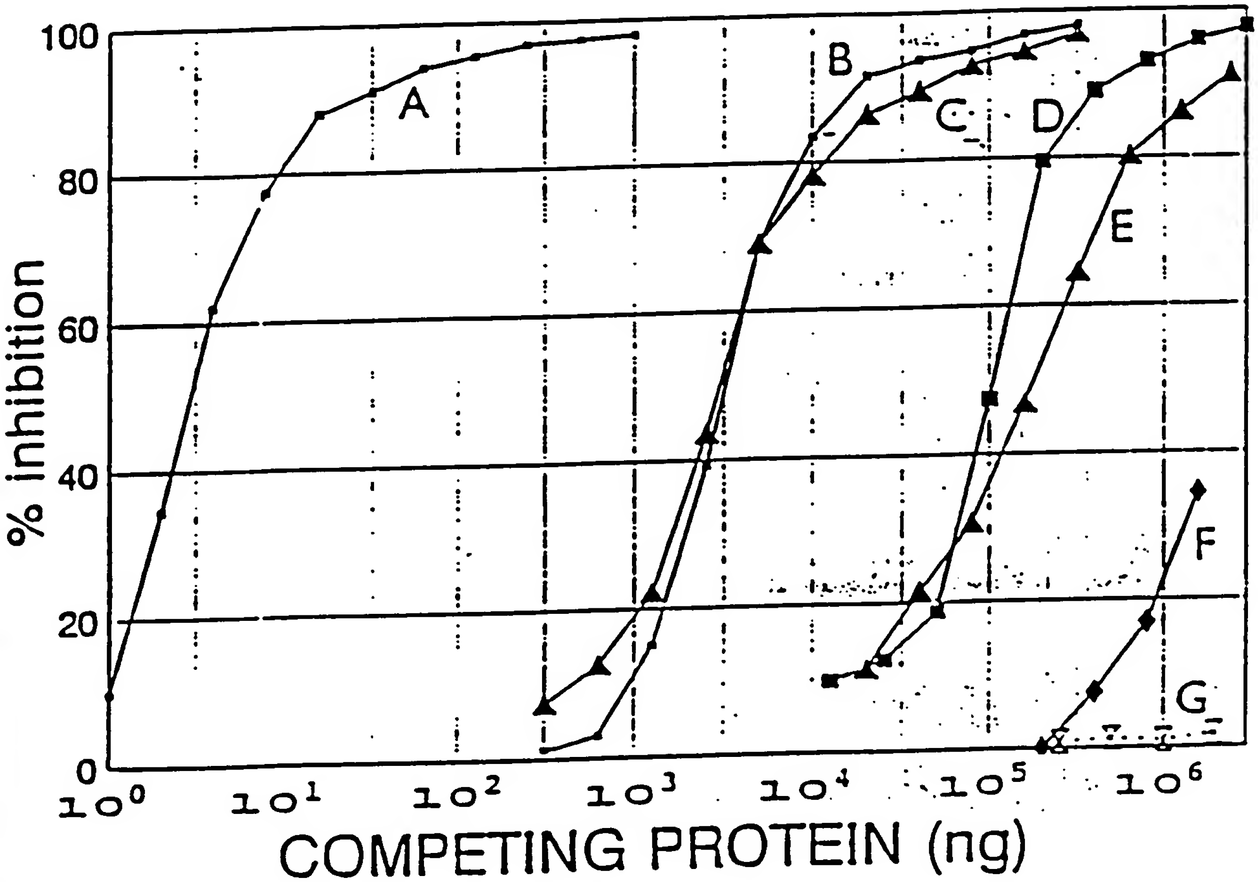

CPM x 10^{-3} PRECIPITATED
1.1
1.0
9
8
7
6
5
4
3
2
1
0
A
10^{-4}
10^{-5}
10^{-6}
10^{-7}
10^{-8}
10^{-9}
CPM x 10^{-2} PRECIPITATED
D
B
E
C
F
10^{-2}
10^{-3}
10^{-4}
DILUTION OF ANTIBODY

FIG. 11



100
80
60
40
20
0
% inhibition
A
B
C
D
E
F
G
10^0
10^1
10^2
10^3
10^4
10^5
10^6
COMPETING PROTEIN (ng)

FIG. 12

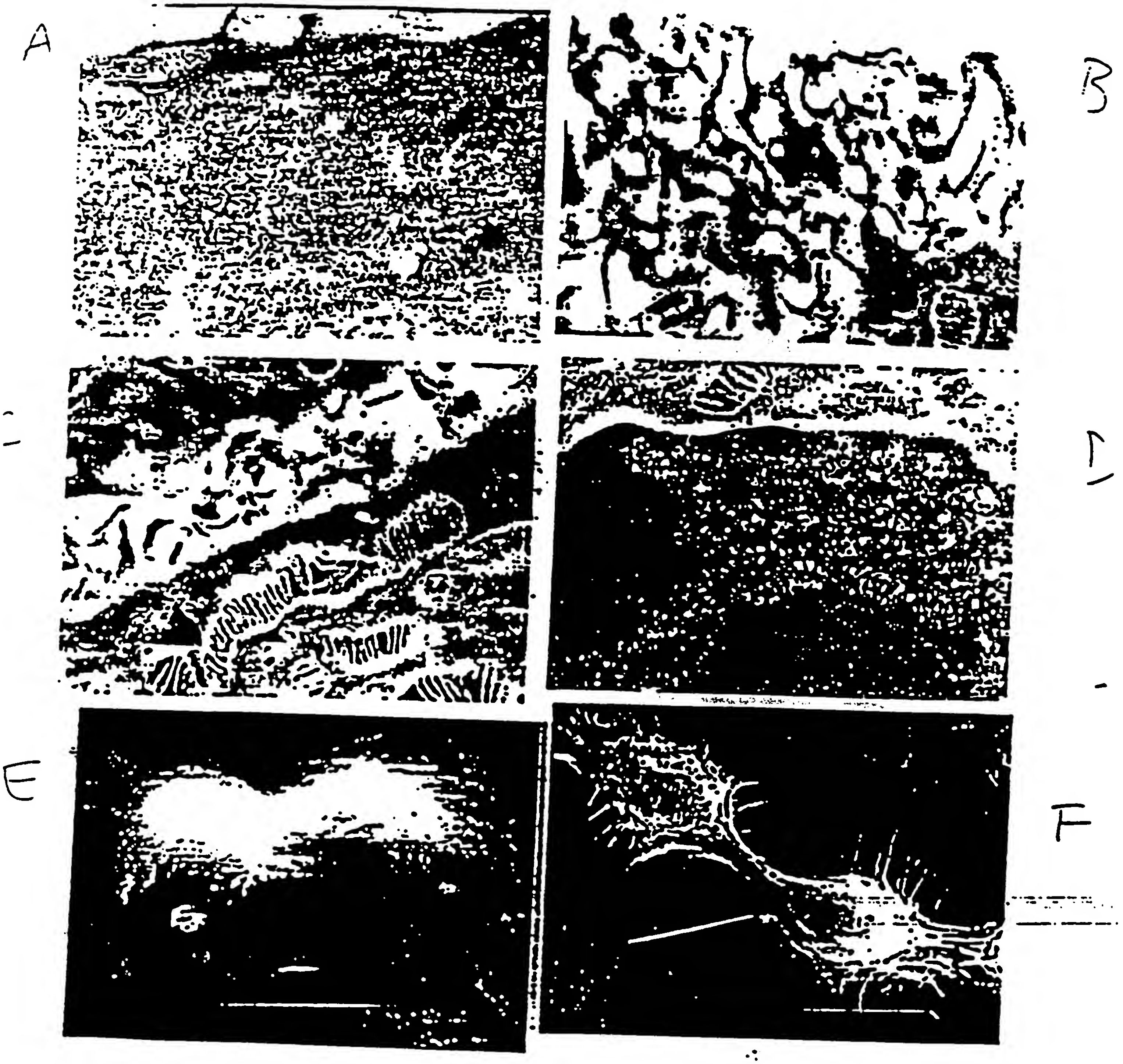


FIG. 13

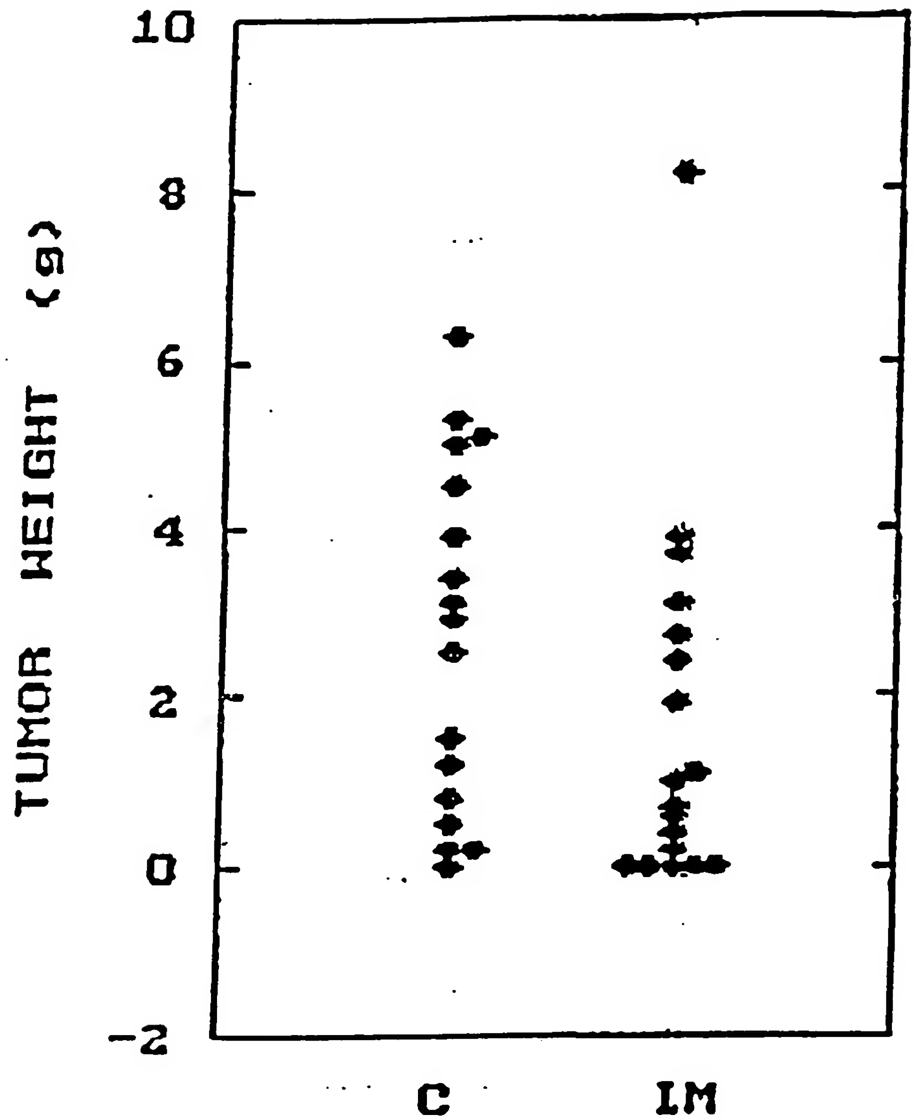


FIG. 14

1 M A P L C P S P V L P L L I P A 16
1 ACAGTCAGCGCATGGCTCCCCTGTGCCCCAGCCCCTGGCTCCCTCTGTTGATCCCGGCCC 60

17 P A P G L T V Q L L L S L L L L M P V H 36
61 CTGCTCCAGGCCTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGATGCCTGTCCATC 120

37 P Q R L P R M Q E D S P L E E A L L G K 56
121 CCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGAGGAGGCTCTTCTGGGGAAGA 180

57 M T H W A R R I C P V K R I H P E R R I 76
181 TGACCCACTGGGCCAGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGAGGAGGATCC 240

77 H P E R R I Y L E R R I Y L E R R I Y L 96
241 ACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGA 300

97 K L M P K S E E E G S L K L E D L P T V 116
301 AGTTAATGCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTTG 360

117 E A P G D P Q E P Q N N A H R D K E G D 136
361 AGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAGGGGATG 420

137 D Q S H W R Y G G D P P G F G C P Q P A 156
421 ACCAGAGTCATTGGCGCTATGGAGCCGACCCGCCTGGCCCCGGGTGTCCCCAGCCTGCGC 480

157 R A A S S P R W I S A P S S P P S A R P 176
481 GGGCCGCTTCCAGTCCCCGGTGGATATCCGCCCCCAGCTCGCCGCCTTCTGCCCGGCCCT 540

177 C A P W N S W A S S S R R S Q N C A C R 196
541 GCGCCCCCTGGAACTCCTGGGCTTCCAGCTCCCGCCGCTCCCAGAACTGCGCCTGCAGAC 600

197 Q W P Q C A T D P A S W A R D G S G S R 216
601 AATGGCCACAGTGTGCAACTGACCCTGCCTCCTGGGCTAGAGATGGCTCTGGGTCCCCGG 660

217 A G V P A L Q L H L N W G A A G R P G S 236
661 CCGGAGTACCGGCTCTGCAGCTGCATCTGCACTGGGGGGCTGCAGGTCGTCCGGGCTCGG 720

237 E H T V E G H R F P A E I H V V H L S T 256
721 ACCACACTGTGGAAGGCCACCGTTTCCCTGCCCAGATCCACGTGGTTCACCTCAGCACCC 780

257 A F A R V D E A L G R P G G L A V L A P 276
781 CCTTTGCCAGAGTTGACGAGGCCCTTGGGCGCCCCGGCAGGCCTGGCCGTGTTGGCCCTT 840

277 F W R R A R K K T V S Y E Q L L S R L E 296
841 TCTCCAGGAGGCCCGGAAGAAAACAGTGTCCTATGAGCAGTTGCTGTCTCGCCTTGGAAG 900

297 E I A E E G S E T Q V P G L D I S A L L 316
901 AAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTCCTGC 960

317 P S D F S R Y F Q Y E G S L T T P P C A 336
961 CCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGTGCCC 1020

337 Q G V I W T V F N Q T V N L S A K Q L H 356
1021 AGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGAATCTGAGTGCCAAGCAGCTCCACA 1080

357 T L S D T L W G P G D S R L Q L N F R A 376
1081 CCCTCTCTGACACCCTGTGGGGCCCTGGTGACTCTCGGCTACAGCTGAACTTCCGAGCGA 1140

377 T Q P L N G R V I E A S F P A G V D S S 396
1141 CGCAGCCTTTGAATGGGCGAGTGATTGAGGCCTCCTTCCCTGCTGGAGTGGACAGCAGTC 1200

397 P R A A E P V Q L N S C L A A G D I L A 416
1201 CTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCCTGGCTGCTGGTGACATCCTAGCCC 1260

417 L V F G L L F A V T S V A F L V Q M R R 436
1261 TGGTTTTTGGCCTCCTTTTTGCTGTCACCAGCGTCGCCTTCCTTGTGCAGATGAGAAGGC 1320

437 Q H R R G T K G G V S V P P S R C S R D 456
1321 AGCACAGAAGGGGAACCAAAGGCGGTGTGAGCGTACCGCCCAGCAGATGTAGCCGAGACT 1380

457 W S L E A G S W R M * 466
1381 CGAGCCTAGAGGCTGGATCTTGGAGAATGTCAGAAGCCAGCCAGAGGCATCTGAGCGGGA 1440

1441 GCCGGTAACTGTCCTGTCCTGCTCATTATCCCACTTCCTTTTAACTGCCAAGAAATTTTT 1500

1501 TAAAATAAATATTTATAAT 1519

FIG. 15

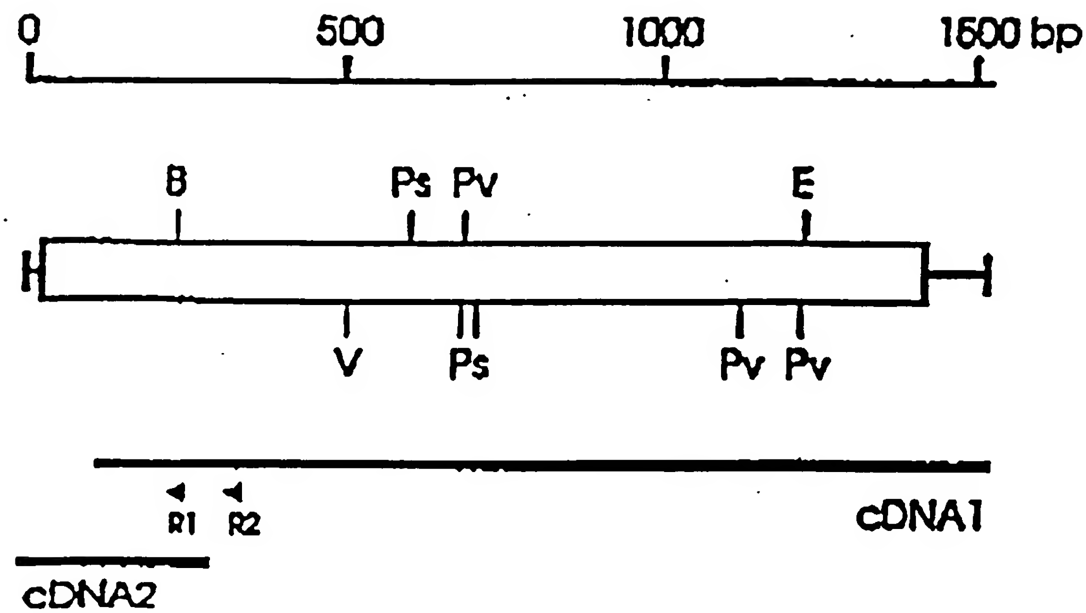


FIG. 16

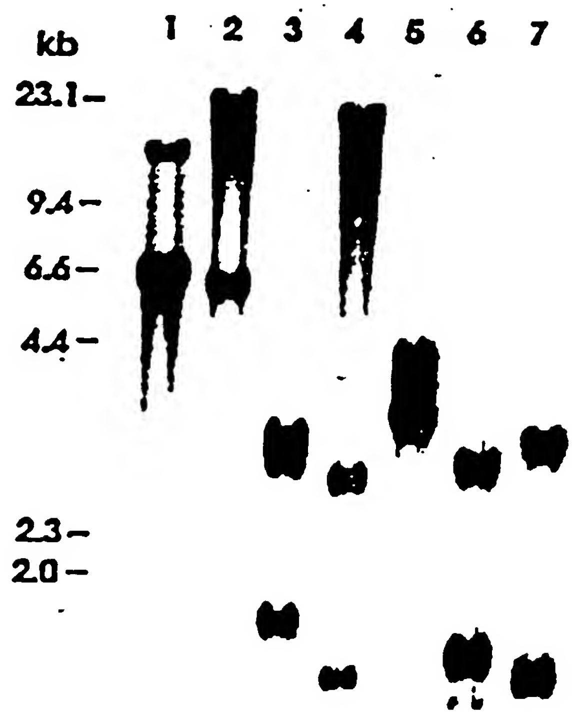


FIG. 17

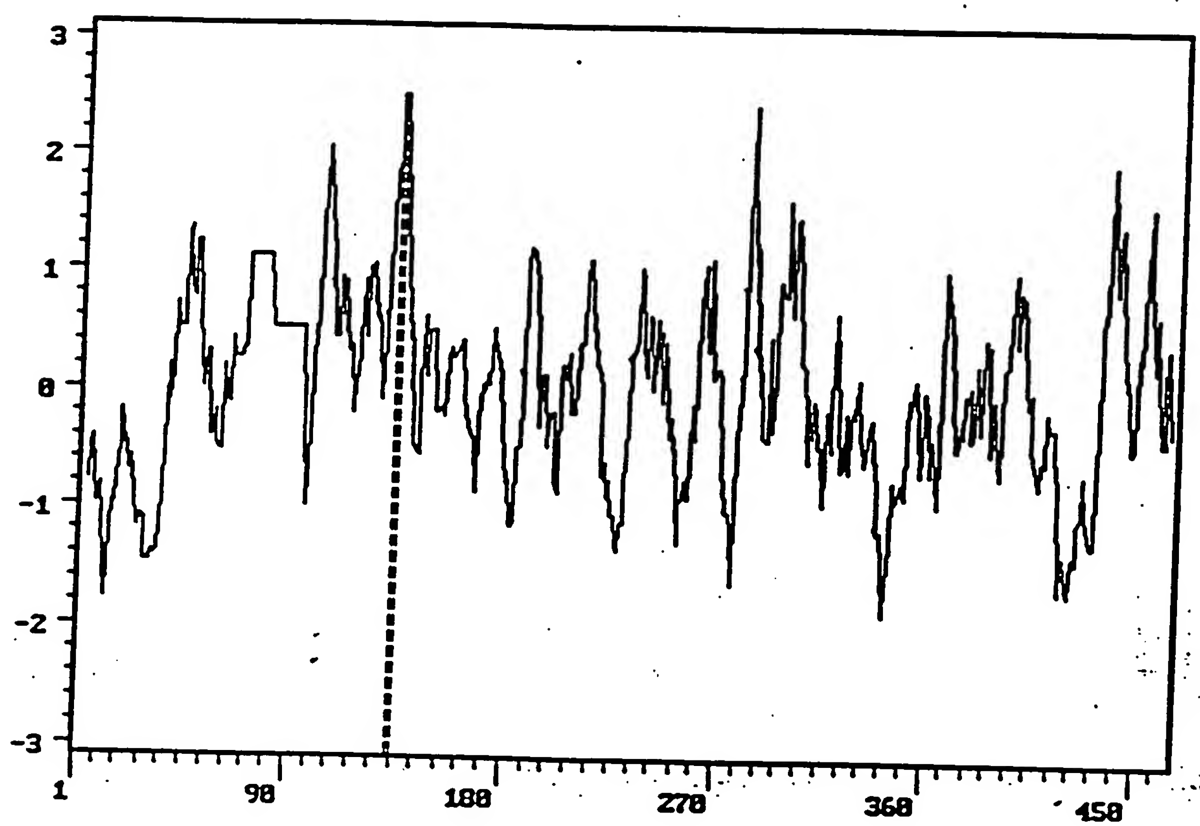


Fig. 18

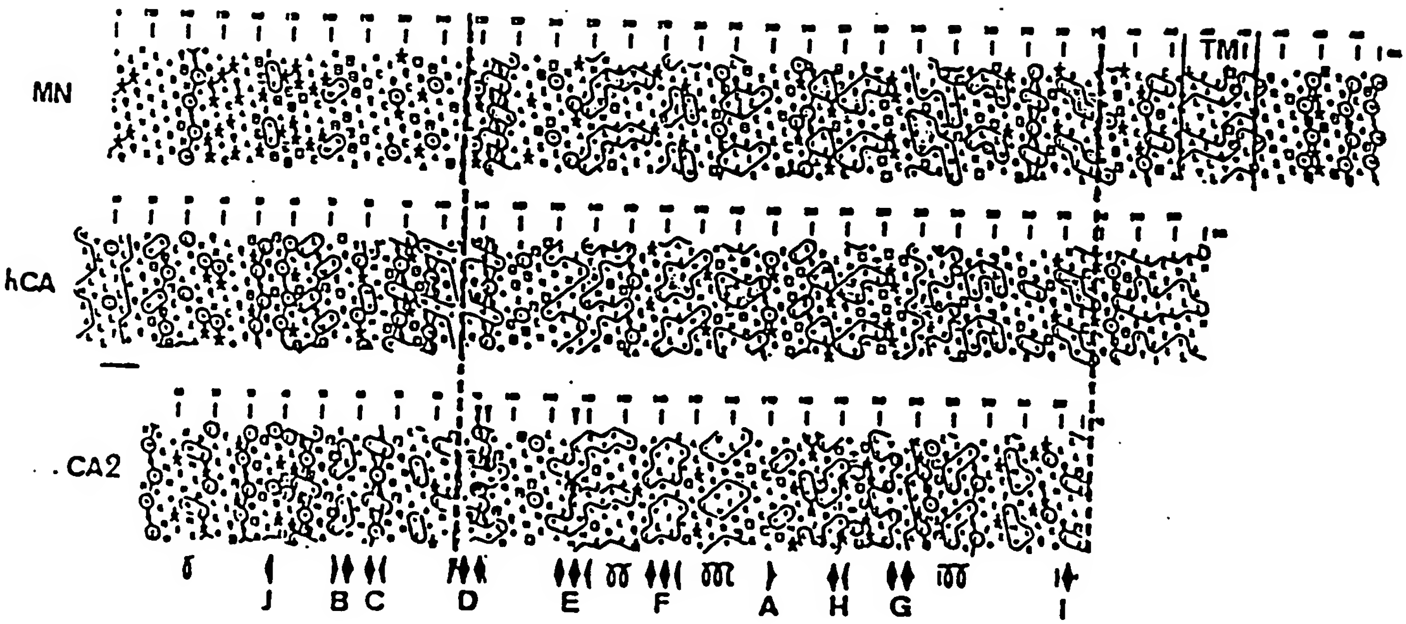


Fig. 19a

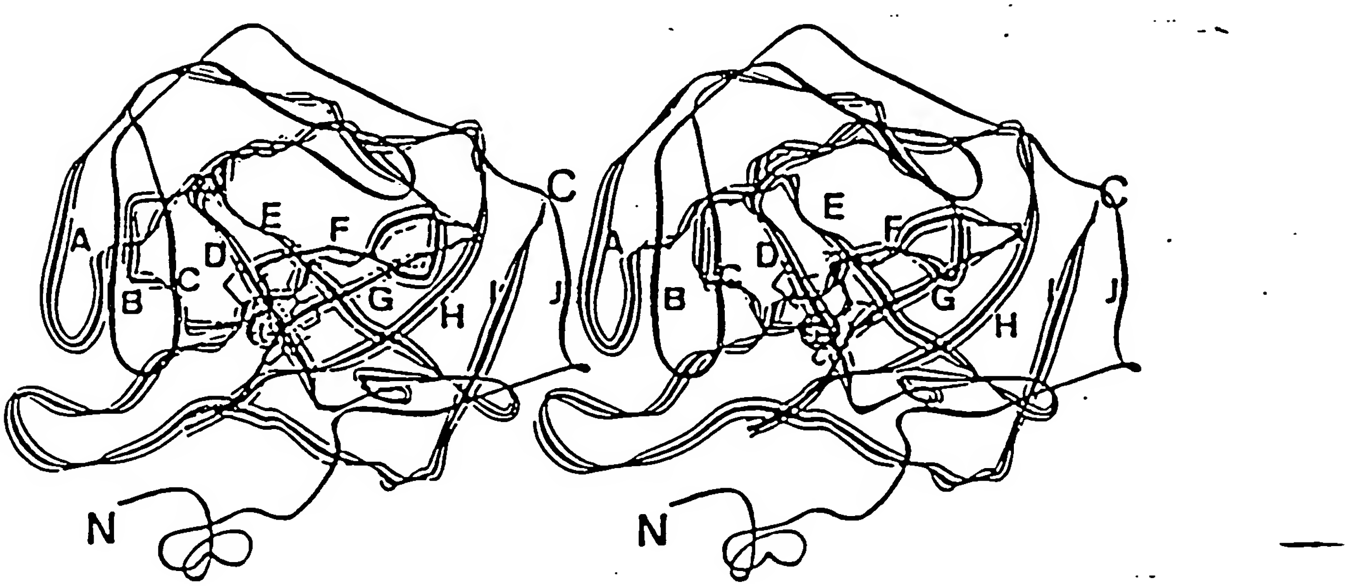


Fig. 19b

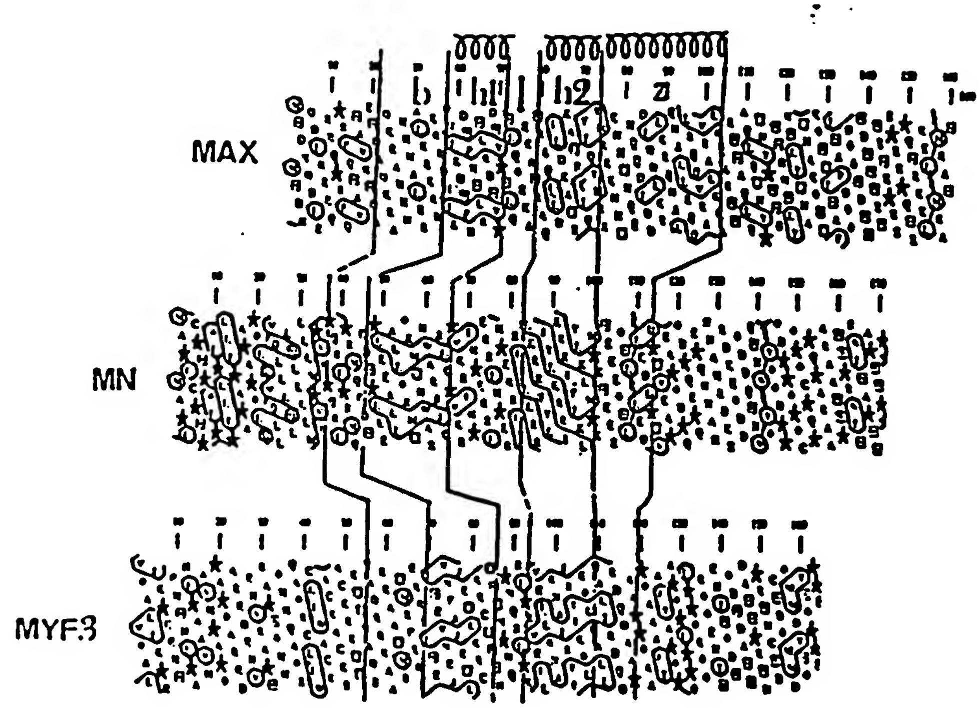


Fig. 19c

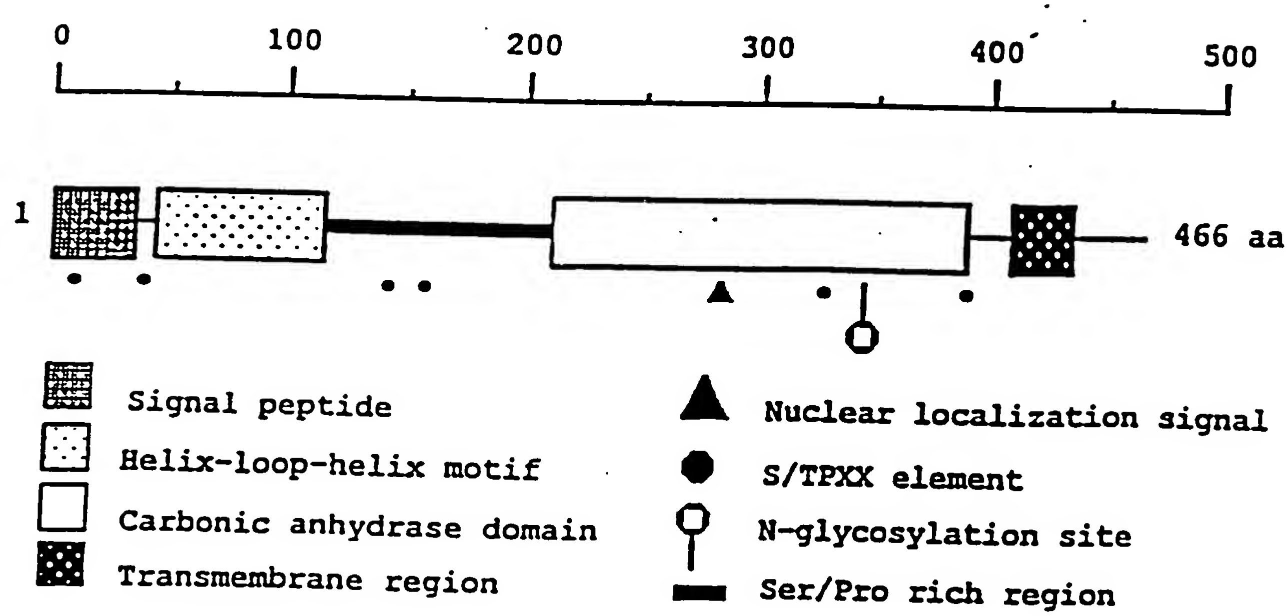


Fig. 19d

MN Promoter Region

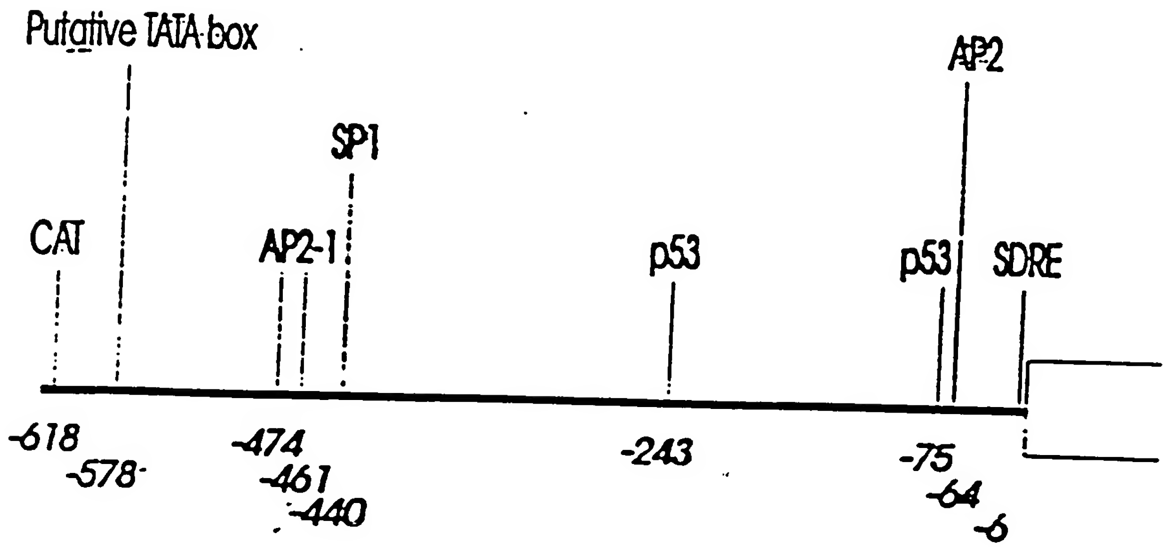


Fig. 20

5' MN Genomic Region

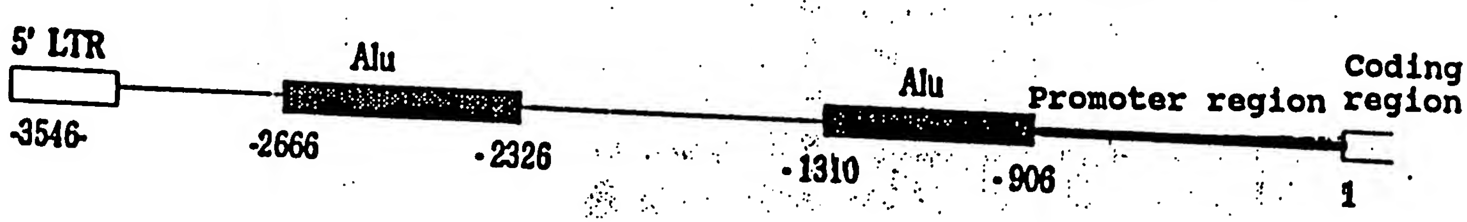


Fig. 21

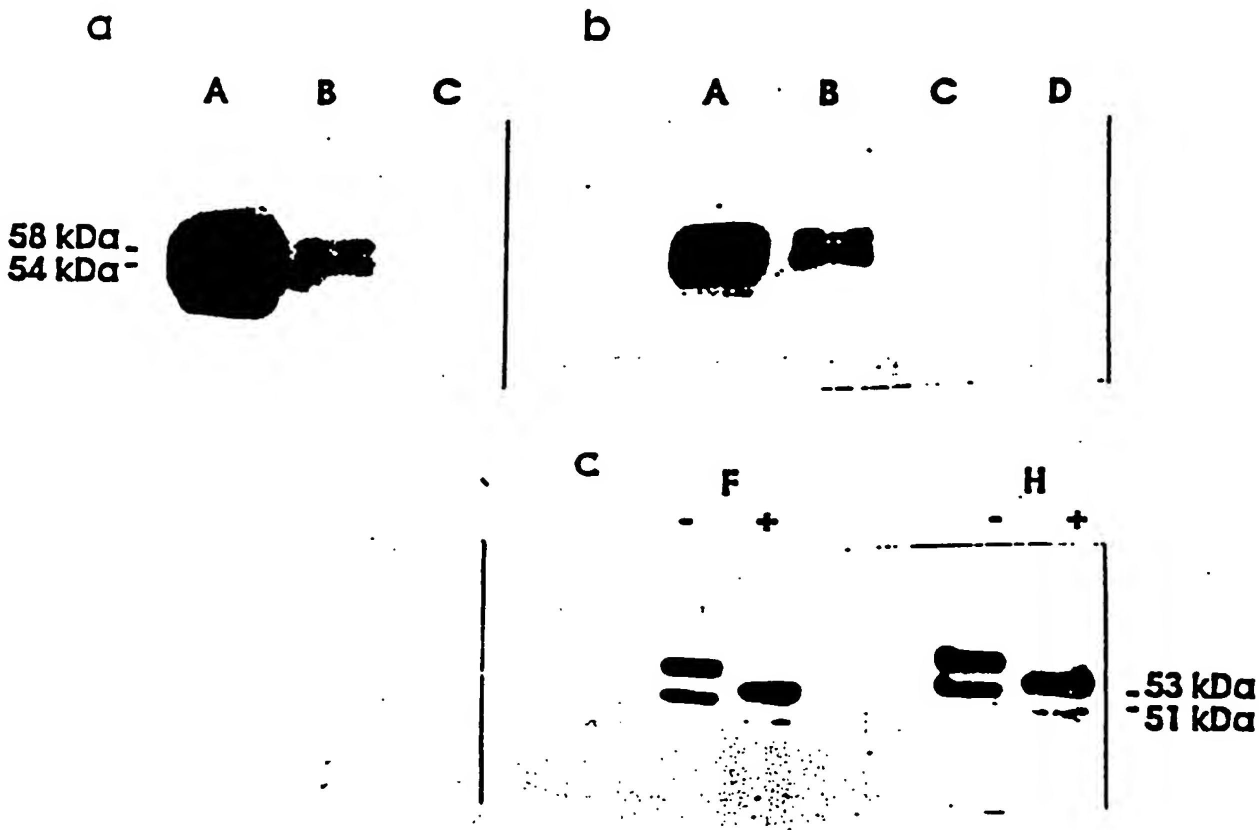
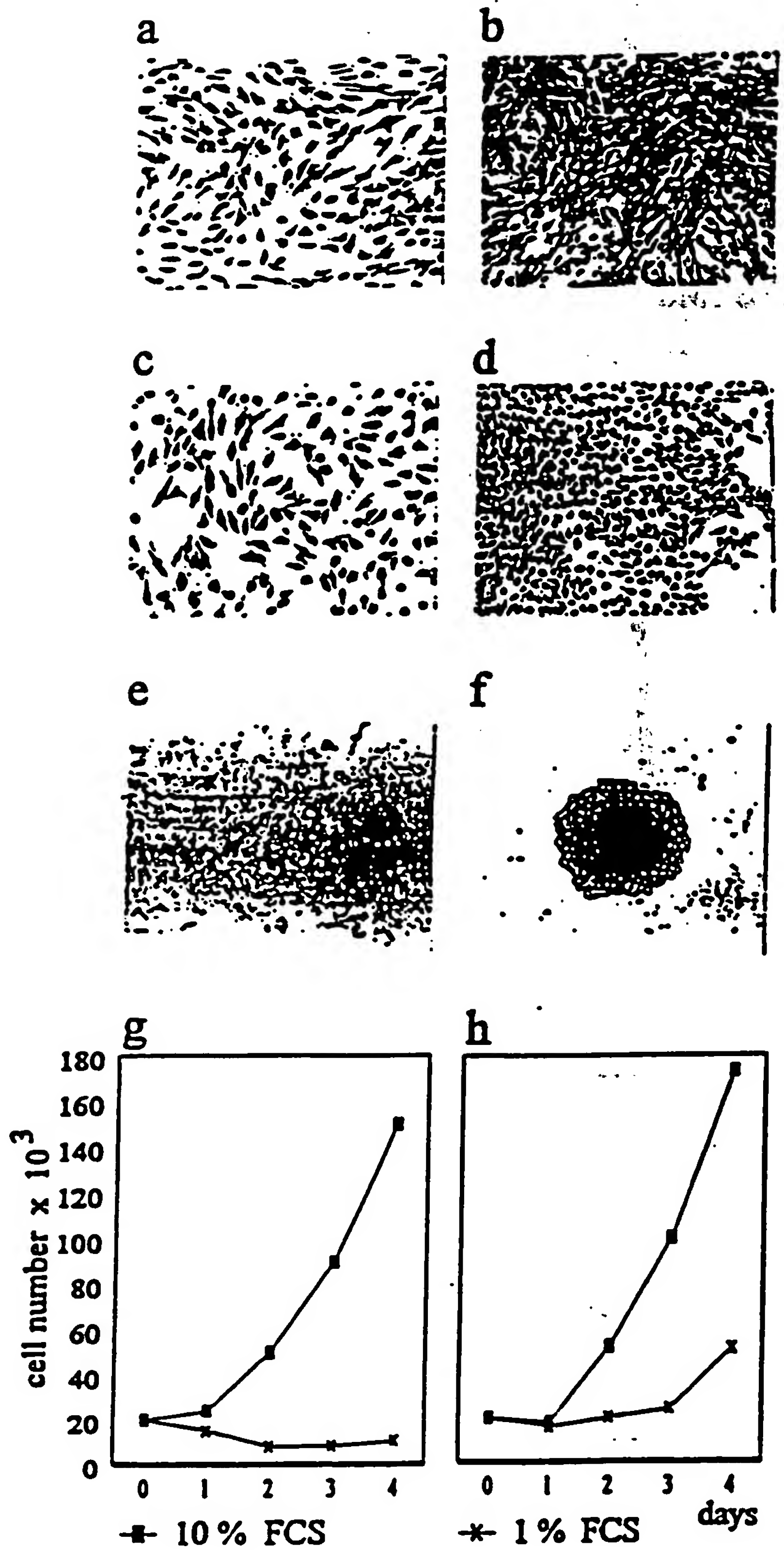
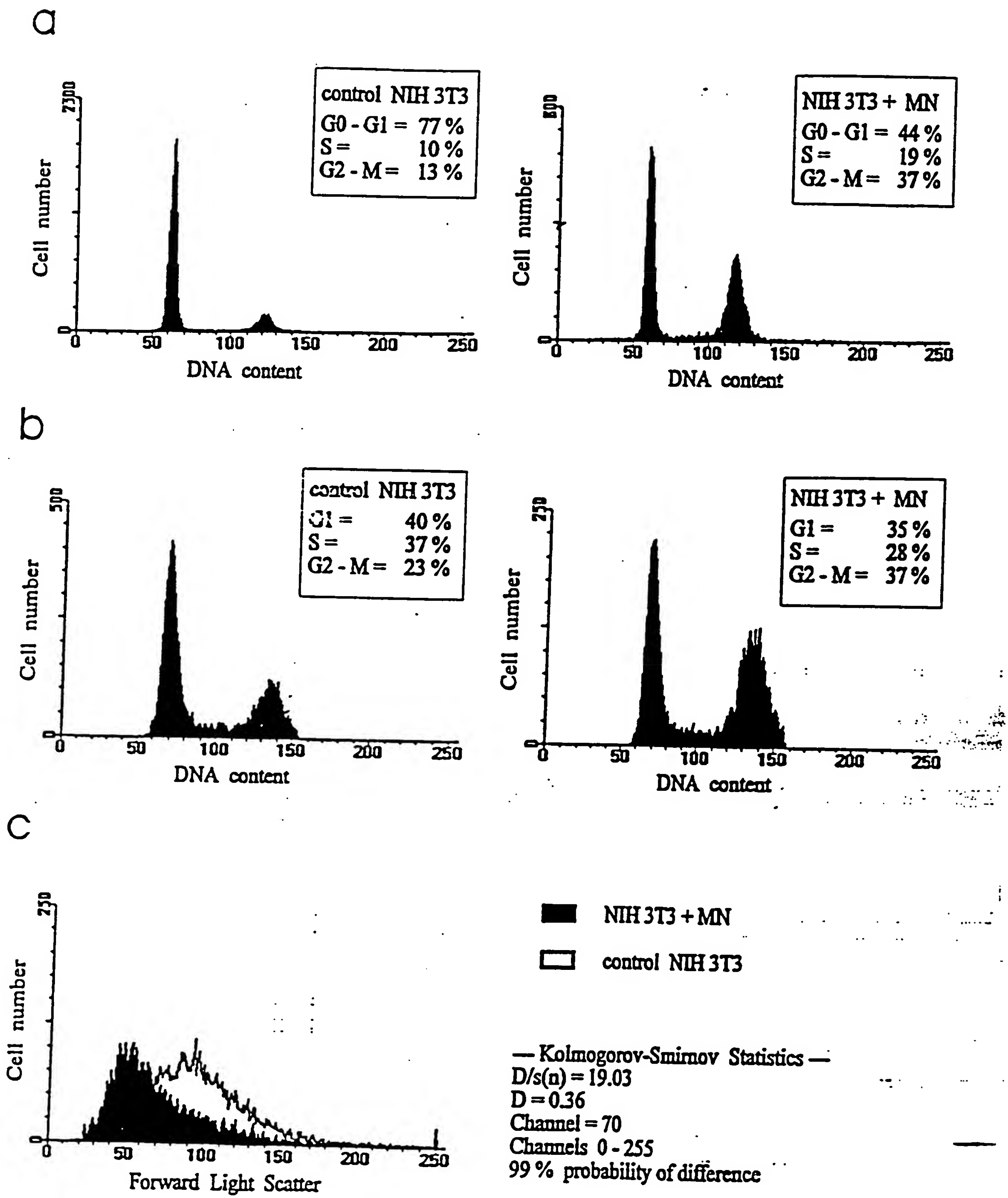


Fig. 22



a
b
c
d
e
f
g
h
180
160
140
120
100
80
60
40
20
0
cell number x 10³
0
1
2
3
4
days
10 % FCS
1 % FCS

Fig. 23



a
control NIH 3T3
G0 - G1 = 77 %
S = 10 %
G2 - M = 13 %
Cell number
DNA content
0
50
100
150
200
250
NIH 3T3 + MN
G0 - G1 = 44 %
S = 19 %
G2 - M = 37 %
b
control NIH 3T3
G1 = 40 %
S = 37 %
G2 - M = 23 %
NIH 3T3 + MN
G1 = 35 %
S = 28 %
G2 - M = 37 %
c
NIH 3T3 + MN
control NIH 3T3
Forward Light Scatter
— Kolmogorov-Smirnov Statistics —
D/s(n) = 19.03
D = 0.36
Channel = 70
Channels 0 - 255
99 % probability of difference

Fig. 24

SQ Sequence 5052 BP; 1201 A; 1249 C; 1201 G; 1399 T.

GGATCCTGTT GACTCGTGAC CTTACCCCCA ACCCTGTGCT CTCTGAAACA TGAGCTGTGT
CCACTCAGGG TTAAATGGAT TAAGGGCGGT GCAAGATGTG CTTTGTTAAA CAGATGCTTG
AAGGCAGCAT GCTCGTTAAG AGTCATCACC AATCCCTAAT CTCAAGTAAT CAGGGACACA
AACACTGCGG AAGGCCGCAG GGTCCTCTGC CTAGGAAAAC CAGAGACCTT TGTTCACTTG
TTTATCTGAC CTTCCCTCCA CTATTGTCCA TGACCCTGCC AAATCCCCCT CTGTGAGAAA
CACCCAAGAA TTATCAATAA AAAAATAAAT TTAAAAAAAA AATACAAAAA AAAAAAAAAA
AAAAAAAAAA GACTTACGAA TAGTTATTGA TAAATGAATA GCTATTGGTA AAGCCAAGTA
AATGATCATA TTCAAAACCA GACGGCCATC ATCACAGCTC AAGTCTACCT GATTTGATCT
CTTTATCATT GTCATTCTTT GGATTCACTA GATTAGTCAT CATCCTCAAA ATTCTCCCCC
AAGTTCTAAT TACGTTCCAA ACATTTAGGG GTTACATGAA GCTTGAACCT ACTACCTTCT
TTGCTTTTGA GCCATGAGTT GTAGGAATGA TGAGTTTACA CCTTACATGC TGGGGATTAA
TTTAAACTTT ACCTCTAAGT CAGTTGGGTA GCCTTTGGCT TATTTTTGTA GCTAATTTTG
TAGTTAATGG ATGCACTGTG AATCTTGCTA TGATAGTTTT CCTCCACACT TTGCCACTAG
GGGTAGGTAG GTACTCAGTT TTCAGTAATT GCTTACCTAA GACCCTAAGC CCTATTTCTC
TTGTACTGGC CTTTATCTGT AATATGGGCA TATTTAATAC AATATAATTT TTGGAGTTTT
TTTGTTTGTT TGTTTGTTTG TTTTTTTGAG ACGGAGTCTT GCATCTGTCA TGCCCAGGCT
GGAGTAGCAG TGGTGCCATC TCGGCTCACT GCAAGCTCCA CCTCCCGAGT TCACGCCATT
TTCCTGCCTC AGCCTCCCGA GTAGCTGGGA CTACAGGCGC CCGCCACCAT GCCCGGCTAA
TTTTTTGTAT TTTTGGTAGA GACGGGGTTT CACCGTGTTA GCCAGAATGG TCTCGATCTC
CTGACTTCGT GATCCACCCG CCTCGGCCTC CCAAAGTTCT GGGATTACAG GTGTGAGCCA
CCGCACCTGG CCAATTTTTT GAGTCTTTTA AAGTAAAAAT ATGTCTTGTA AGCTGGTAAC
TATGGTACAT TTCCTTTTAT TAATGTGGTG CTGACGGTCA TATAGGTTCT TTTGAGTTTG
GCATGCATAT GCTACTTTTT GCAGTCCTTT CATTACATTT TTCTCTCTTC ATTTGAAGAG
CATGTTATAT CTTTTAGCTT CACTTGGCTT AAAAGGTTCT CTCATTAGCC TAACACAGTG
TCATTGTTGG TACCACTTGG ATCATAAGTG GAAAAACAGT CAAGAAATTG CACAGTAATA
CTTGTTTGTA AGAGGGATGA TTCAGGTGAA TCTGACACTA AGAAACTCCC CTACCTGAGG
TCTGAGATTC CTCTGACATT GCTGTATATA GGCTTTTCCT TTGACAGCCT GTGACTGCGG
ACTATTTTTC TTAAGCAAGA TATGCTAAAG TTTTGTGAGC CTTTTTCCAG AGAGAGGTCT
CATATCTGCA TCAAGTGAGA ACATATAATG TCTGCATGTT TCCATATTTC AGGAATGTTT
GCTTGTGTTT TATGCTTTTA TATAGACAGG GAAACTTGTT CCTCAGTGAC CCAAAAGAGG
TGGGAATTGT TATTGGATAT CATCATTGGC CCACGCTTTC TGACCTTGGA AACAATTAAG
GGTTCATAAT CTCAATTCTG TCAGAATTGG TACAAGAAAT AGCTGCTATG TTTCTTGACA
TTCCACTTGG TAGGAAATAA GAATGTGAAA CTCTTCAGTT GGTGTGTGTC CCTNGTTTTT
TTGCAATTTC CTTCTTACTG TGTTAAAAAA AAGTATGATC TTGCTCTGAG AGGTGAGGCA
TTCTTAATCA TGATCTTTAA AGATCAATAA TATAATCCTT TCAAGGATTA TGTCTTTATT
ATAATAAAGA TAATTTGTCT TTAACAGAAT CAATAATATA ATCCCTTAAA GGATTATATC
TTTGCTGGGC GCAGTGGCTC ACACCTGTAA TCCCAGCACT TTGGGTGGCC AAGGTGGAAG
GATCAAATTT GCCTACTTCT ATATTATCTT CTAAAGCAGA ATTCATCTCT CTTCCCTCAA
TATGATGATA TTGACAGGGT TTGCCCTCAC TCACTAGATT GTGAGCTCCT GCTCAGGGCA
GGTAGNGTTT TTTGTTTTTG TTTTTGTTTT TCTTTTTTGA GACAGGGTCT TGCTCTGTCA
CCCAGGCCAG AGTGCAATGG TACAGTCTCA GCTCACTGCA GCCTCAACGC CTCGGCTCAA
ACCATCATCC CATTTCAGCC TCCTGAGTAG CTGGGACTAC AGGCACATGC CATTACACCT

Fig. 25a

GGCTAATTTT TTTGTATTTC TAGTAGAGAC AGGGTTTGGC CATGTTGCCC GGGCTGGTCT
CGAACTCCTG GACTCAAGCA ATCCACCCAC CTCAGCCTCC CAAAATGAGG GACCGTGTCT
TATTCATTTC CATGTCCCTA GTCCATAGCC CAGTGCTGGA CCTATGGTAG TACTAAATAA
ATATTTGTTG AATGCAATAG TAAATAGCAT TTCAGGGAGC AAGAACTAGA TTAACAAAGG
TGGTAAAAGG TTTGGAGAAA AAAATAATAG TTTAATTTGG CTAGAGTATG AGGGAGAGTA
GTAGGAGACA AGATGGAAAG GTCTCTTGGG CAAGGTTTTG AAGGAAGTTG GAAGTCAGAA
GTACACAATG TGATATCGTG GCAGGCAGTG GGGAGCCAAT GAAGGCTTTT GAGCAGGAGA
GTAATGTGTT GAAAAATAAA TATAGGTTAA ACCTATCAGA GCCCCTCTGA CACATACACT
TGCTTTTCAT TCAAGCTCAA GTTTGTCTCC CACATACCCA TTACTTAACT CACCCTCGGG
CTCCCCTAGC AGCCTGCCCT ACCTCTTTAC CTGCTTCCTG GTGGAGTCAG GGATGTATAC
ATGAGCTGCT TTCCCTCTCA GCCAGAGACA TGGGGGGCCC CAGCTCCCCT GCCTTTCCCC
TTCTGTGCCT GGAGCTGGGA AGCAGGCCAG GGTTAGCTGA GGCTGGCTGG CAAGCAGCTG
GGTGGTGCCA GGGAGAGCCT GCATAGTGCC AGGTGGTGCC TTGGGTTCCA AGCTAGTCCA
TGGCCCCGAT AACCTTCTGC CTGTGCACAC ACCTGCCCCT CACTCCACCC CCATCCTAGC
TTTGGTATGG GGGAGAGGGC ACAGGGCCAG ACAAACCTGT GAGACTTTGG CTCCATCTCT
GCAAAAGGGC GCTCTGTGAG TCAGCCTGCT CCCCTCCAGG CTTGCTCCTC CCCCACCCAG
CTCTCGTTTC CAATGCACGT ACAGCCCGTA CACACCGTGT GCTGGGACAC CCCACAGTCA
GCGCATGGCT CCCCTGTGCC CCAGCCCCTG GCTCCCTCTG TTGATCCCGG CCCCTGCTCC
AGGCCTCACT GTGCAACTGC TGCTGTCACT GCTGCTTCTG ATGCCTGTCC ATCCCCAGAG
GTTGCCCCGG ATGCAGGAGG ATTCCCCCTT GGAGGAGGCT CTTCTGGGGA AGATGACCCA
CTGGGCGAGG AGGATCTGCC CAGTGAAGAG GATTCACCCA GAGAGGAGGA TCCACCCGGA
GAGGAGGATC TACCTGGAGA GGAGGATCTA CCTGGAGAGG AGGATCTACC TGAAGTTAAT
GCCTAAATCA GAAGAAGAGG GCTCCCTGAA GTTAGAGGAT CTACCTACTG TTGAGGCTCC
TGGAGATCCT CAAGAACCCC AGAATAATGC CCACAGGGAC AAAGAAGGGG ATGACCAGAG
TCATTGGCGC TATGGAGGCG ACCCGCCTGG CCCCGGGTGT CCCCAGCCTG CGCGGGCCGC
TTCCAGTCCC CGGTGGATAT CCGCCCCCAG CTCGCCGCCT TCTGCCCGGC CCTGCGCCCC
CTGGAACTCC TGGGCTTCCA GCTCCCGCCG CTCCCAGAAC TGCGCCTGCA GACAATGGCC
ACAGTGTGCA ACTGACCCTG CCTCCTGGGC TAGAGATGGC TCTGGGTCCC GGGCGGGAGT
ACCGGCTCTG CAGCTGCATC TGCACTGGGG GGCTGCAGGT CGTCCGGGCT CGGAGCACAC
TGTGGAAGGC CACCGTTTCC CTGCCGAGAT CCACGTGGTT CACCTCAGCA CCGCCTTTGC
CAGAGTTGAC GAGGCCTTGG GGCGCCCGGG AGGCCTGGCC GTGTTGGCGC CTTTCTGGAG
GAGGGCCCGG AAGAAAACAG TGTCCTATGA GCAGTTGCTG TCTCGCTTGG AAGAAATCGC
TGAGGAAGGC TCAGAGACTC AGGTCCCAGG ACTGGACATA TCTGCACTCC TGCCCTCTGA
CTTCAGCCGC TACTTCCAAT ATGAGGGGTC TCTGACTACA CCGCCCTGTG CCCAGGGTGT
CATCTGGACT GTGTTTAACC AGACAGTGAT GCTGAGTGCT AAGCAGCTCC ACACCCTCTC
TGACACCCTG TGGGGACCTG GTGACTCTCG GCTACAGCTG AACTTCCGAG CGACGCAGCC
TTTGAATGGG CGAGTGATTG AGGCCTCCTT CCCTGCTGGA GTGGACAGCA GTCCTCGGGC
TGCTGAGCCA GTCCAGCTGA ATTCCTGCCT GGCTGCTGGT GACATCCTAG CCCTGGTTTT
TGGCCTCCTT TTTGCTGTCA CCAGCGTCGC GTTCCTTGTG CAGATGAGAA GGCAGCACAG
AAGGGGAACC AAAGGGGGTG TGAGCGTACC GCCCAGCAGA GGTAGCCGAG ACTGGAGCCT
AGAGGCTGGA TCTTGGAGAA TGTGAGAAGC CAGCCAGAGG CATCTGAGGG GGAGCCGGTA
ACTGTCCTGT CCTGCTCATT ATGCCACTTC CTTTTAACTG CCAAGAAATT TTTTAAAATA
AATATTTATA AT
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Fig. 25b